



FIG.1A

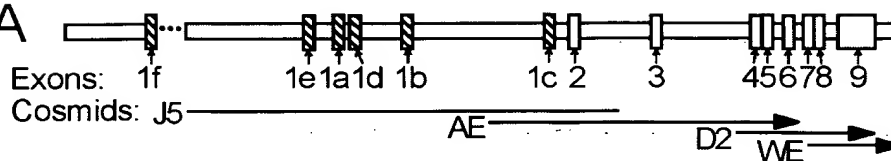
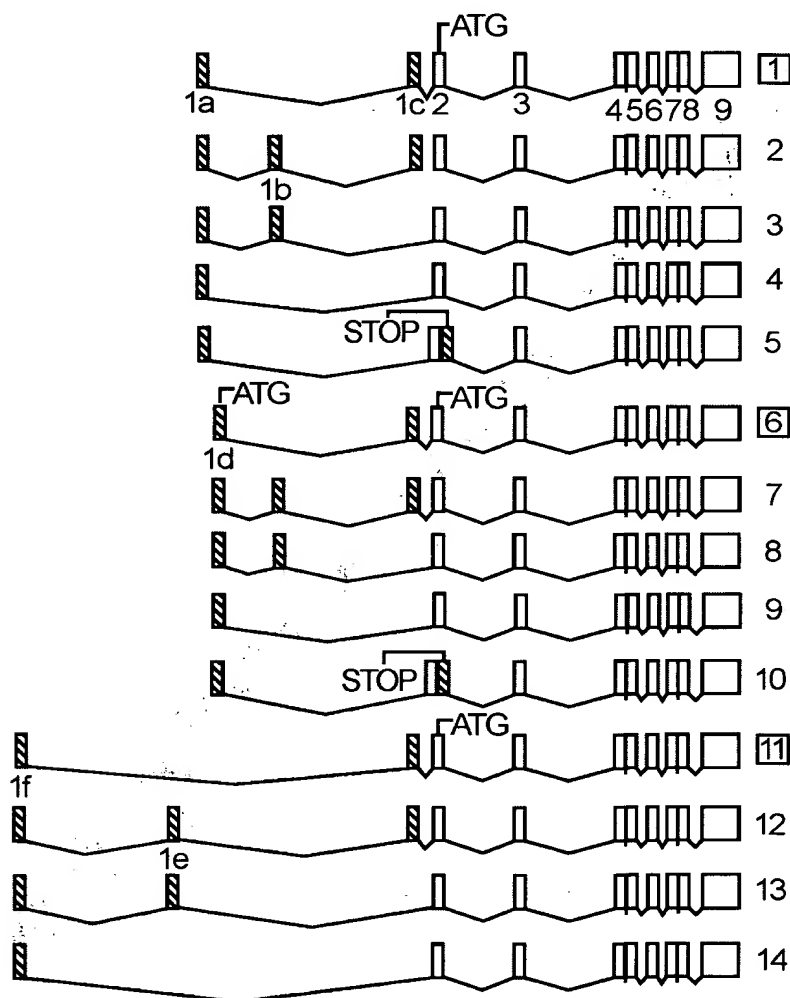


FIG.1B



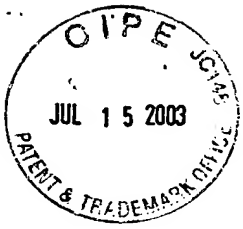
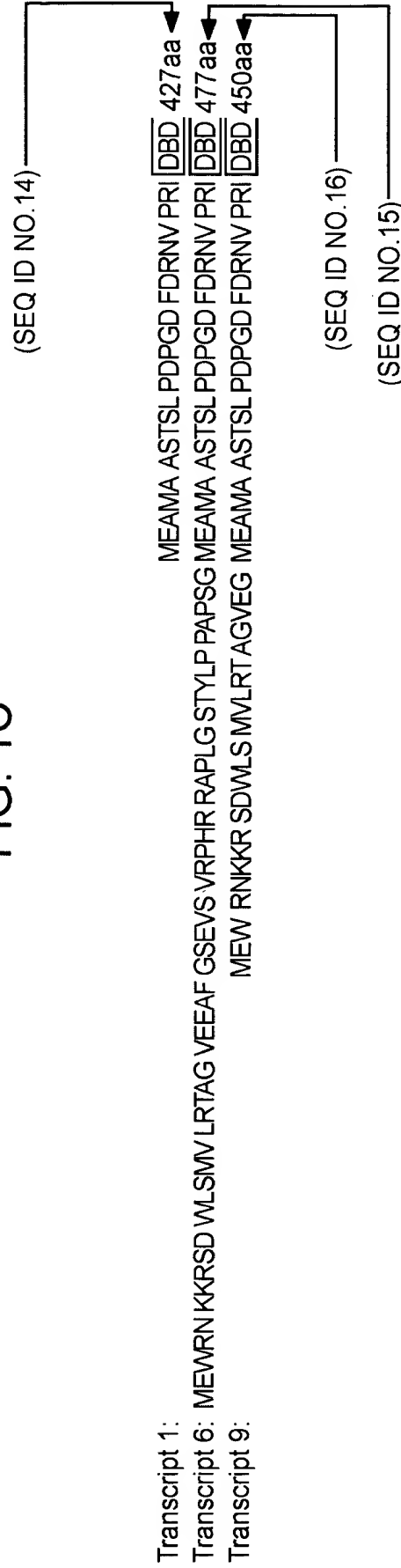


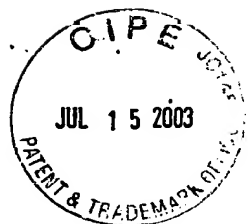
FIG. 1C





## FIG. 4

- A. 5'...atcccttaag GGCTCCTGAACCTAGCCCAGCTGGACGGAG  
AAATGGACTCTAGCCTCCTCTGATAGCCTCATGCCAGGCC  
CGTGCACATTGCTTTGCTTGCCTCCCTCAATCCTCATAGCT  
TCTCTTTGGGgtaagtacag...3' (SEQ ID NO: 13)
- B. 5'...TGCGACCTTGGCGGTGAGCCTGGGGACAGGGGTGAGGC  
CAGAGACGGACGGACGCAGGGGCCCCGGCCCAAGGCGAGGG  
AGAACAGCGGCACTAAGGCAGAAAGGAAGAGGGCGGTGTG  
TTCACCCGCAGCCCAATCCATCACTCAGCAACTCCTAGAC  
GCTGGTAGAAAGTTCTCCGAGGAGCCTGCCATCCAGTCGT  
GCGTGCAG...3' (SEQ ID NO: 5)
- C. 5'...tgtttttag AGGCAGCATGAAACAGTGGGATGTGCAGAG  
AGAAGATCTGGGTCCAGTAGCTCTGACACTCCTCAGCTGT  
AGAAACCTTGACAACTCTGCACATCAGTTGTACAATGGAA  
CGGTATTTTTTACTCTTCATGTCTGAAAAGGCTATGATAA  
AGATCAAgttaagatatt...3' (SEQ ID NO: 6)
- D. 5'...GTTTCCTTCTTCTGTGCGGGGCGCCTTGGCATGGAGTGG  
AGGAATAAGAAAAGGAGCGATTGGCTGTGCGATGGTGCTCA  
GAACTGCTGGAGTGGAGGgtgtgtaacc...3' (SEQ ID NO: 1)



## FIG. 5A

### Transcript 6

(Sequence Range: 1 to 1463)

```

      10      20      30      40      50
      *      *      *      *      *
GTTTCCTTCT TCTGTCGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
                                   MetGluTrpArg AsnLysLys>

      60      70      80      90     100
      *      *      *      *      *
AGGAGCGATT GGCTGTTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGAAGC
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCTTCG
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGluAla>

     110     120     130     140     150
      *      *      *      *      *
CTTTGGGTCT GAAGTGTCTG TGAGACCTCA CAGAAGAGCA CCCCTGGGCT
GAAACCCAGA CTTACAGAC ACTCTGGAGT GTCTTCTCGT GGGGACCCGA
PheGlySer GluValSer ValArgProHis ArgArgAla ProLeuGly>

     160     170     180     190     200
      *      *      *      *      *
CCACTTACCT GCCCCCTGCT CCTTCAGGGA TGGAGGCAAT GGCGGCCAGC
GGTGAATGGA CGGGGGACGA GGAAGTCCCT ACCTCCGTTA CCGCCGGTCG
SerThrTyrLeu ProProAla ProSerGly MetGluAlaMet AlaAlaSer>

     210     220     230     240     250
      *      *      *      *      *
ACTTCCCTGC CTGACCCTGG AGACTTTGAC CGGAACGTGC CCCGGATCTG
TGAAGGGACG GACTGGGACC TCTGAAACTG GCCTTGCACG GGGCCTAGAC
ThrSerLeu ProAspProGly AspPheAsp ArgAsnVal ProArgIleCys>

     260     270     280     290     300
      *      *      *      *      *
TGGGGTGTGT GGAGACCGAG CCACTGGCTT TCACTTCAAT GCTATGACCT
ACCCACACA CCTCTGGCTC GGTGACCGAA AGTGAAGTTA CGATACTGGA
GlyValCys GlyAspArg AlaThrGlyPhe HisPheAsn AlaMetThr>

     310     320     330     340     350
      *      *      *      *      *
GTGAAGGCTG CAAAGGCTTC TTCAGGCGAA GCATGAAGCG GAAGGCACTA
CACTTCCGAC GTTCCGAAG AAGTCCGCTT CGTACTTCGC CTTCCGTGAT
CysGluGlyCys LysGlyPhe PheArgArg SerMetLysArg LysAlaLeu>

     360     370     380     390     400
      *      *      *      *      *
TTCACCTGCC CCTTCAACGG GGA CTGCGC ATCACCAAGG ACAACCGACG
AAGTGGACGG GGAAGTTGCC CCTGACGGCG TAGTGGTTCC TGTGCTGC
PheThrCys ProPheAsnGly AspCysArg IleThrLys AspAsnArgArg>

```



## FIG. 5B

```

      410      420      430      440      450
      *      *      *      *      *
CCACTGCCAG GCCTGCCGGC TCAAACGCTG TGTGGACATC GGCATGATGA
GGTGACGGTC CGGACGGCCG AGTTTGCAC ACACCTGTAG CCGTACTACT
  HisCysGln AlaCysArg LeuLysArgCys ValAspIle GlyMetMet>

      460      470      480      490      500
      *      *      *      *      *
AGGAGTTCAT TCTGACAGAT GAGGAAGTGC AGAGGAAGCG GGAGATGATC
TCCTCAAGTA AGACTGTCTA CTCCTTCACG TCTCCTTCGC CCTCTACTAG
LysGluPheIle LeuThrAsp GluGluVal GlnArgLysArg GluMetIle>

      510      520      530      540      550
      *      *      *      *      *
CTGAAGCGGA AGGAGGAGGA GGCCTTGAAG GACAGTCTGC GGCCCAAGCT
GACTTCGCCT TCCTCCTCCT CCGGAAGTTC CTGTCAGACG CCGGGTTCTGA
LeuLysArg LysGluGluGlu AlaLeuLys AspSerLeu ArgProLysLeu>

      560      570      580      590      600
      *      *      *      *      *
GTCTGAGGAG CAGCAGCGCA TCATTGCCAT ACTGCTGGAC GCCCACCATA
CAGACTCCTC' GTCGTCGCGT AGTAACGGTA TGACGACCTG CGGGTGGTAT
  SerGluGlu GlnGlnArg IleIleAlaIle LeuLeuAsp AlaHisHis>

      610      620      630      640      650
      *      *      *      *      *
AGACCTACGA CCCACCTAC TCCGACTTCT GCCAGTTCCG GCCTCCAGTT
TCTGGATGCT GGGGTGGATG AGGCTGAAGA CGGTCAAGGC CGGAGGTCAA
LysThrTyrAsp ProThrTyr SerAspPhe CysGlnPheArg ProProVal>

      660      670      680      690      700
      *      *      *      *      *
CGTGTGAATG ATGGTGGAGG GAGCCATCCT TCCAGGCCCA ACTCCAGACA
GCACACTTAC TACCACCTCC CTCGGTAGGA AGGTCCGGGT TGAGGTCTGT
ArgValAsn AspGlyGlyGly SerHisPro SerArgPro AsnSerArgHis>

      710      720      730      740      750
      *      *      *      *      *
CACTCCCAGC TTCTCTGGGG ACTCCTCCTC CTCCTGCTCA GATCACTGTA
GTGAGGGTCG AAGAGACCCC TGAGGAGGAG GAGGACGAGT CTAGTGACAT
  ThrProSer PheSerGly AspSerSerSer SerCysSer AspHisCys>

      760      770      780      790      800
      *      *      *      *      *
TCACCTCTTC AGACATGATG GACTCGTCCA GCTTCTCCAA TCTGGATCTG
AGTGAGAGAAG TCTGTACTAC CTGAGCAGGT CGAAGAGGTT AGACCTAGAC
IleThrSerSer AspMetMet AspSerSer SerPheSerAsn LeuAspLeu>

      810      820      830      840      850
      *      *      *      *      *
AGTGAAGAAG ATTCAGATGA CCCTTCTGTG ACCCTAGAGC TGTCCCAGCT
TCACTTCTTC TAAGTCTACT GGGAAGACAC TGGGATCTCG ACAGGGTCTGA
SerGluGlu AspSerAspAsp ProSerVal ThrLeuGlu LeuSerGlnLeu>

```



FIG. 5C

```

      860      870      880      890      900
      *      *      *      *      *
CTCCATGCTG CCCCACCTGG CTGACCTGGT CAGTTACAGC ATCCAAAAGG
GAGGTACGAC GGGGTGGACC GACTGGACCA GTCAATGTCG TAGGTTTTC
SerMetLeu ProHisLeu AlaAspLeuVal SerTyrSer IleGlnLys>

      910      920      930      940      950
      *      *      *      *      *
TCATTGGCTT TGCTAAGATG ATACCAGGAT TCAGAGACCT CACCTCTGAG
AGTAACCGAA ACGATTCTAC TATGGTCCTA AGTCTCTGGA GTGGAGACTC
ValIleGlyPhe AlaLysMet IleProGly PheArgAspLeu ThrSerGlu>

      960      970      980      990     1000
      *      *      *      *      *
GACCAGATCG TACTGCTGAA GTCAAGTGCC ATTGAGGTCA TCATGTTGCG
CTGGTCTAGC ATGACGACTT CAGTTCACGG TAACTCCAGT AGTACAACGC
AspGlnIle ValLeuLeuLys SerSerAla IleGluVal IleMetLeuArg>

     1010     1020     1030     1040     1050
      *      *      *      *      *
CTCCAATGAG TCCTTCACCA TGGACGACAT GTCCTGGACC TGTGGCAACC
GAGGTTACTC AGGAAGTGGT ACCTGCTGTA CAGGACCTGG ACACCGTTGG
SerAsnGlu SerPheThr MetAspAspMet SerTrpThr CysGlyAsn>

     1060     1070     1080     1090     1100
      *      *      *      *      *
AAGACTACAA GTACCGCGTC AGTGACGTGA CCAAAGCCGG ACACAGCCTG
TTCTGATGTT CATGGCGCAG TCACTGCACT GGTTCGGGCC TGTGTCCGGAC
GlnAspTyrLys TyrArgVal SerAspVal ThrLysAlaGly HisSerLeu>

     1110     1120     1130     1140     1150
      *      *      *      *      *
GAGCTGATTG AGCCCCTCAT CAAGTTCCAG GTGGGACTGA AGAAGCTGAA
CTCGACTAAC TCGGGGAGTA GTTCAAGGTC CACCCTGACT TCTTCGACTT
GluLeuIle GluProLeuIle LysPheGln ValGlyLeu LysLysLeuAsn>

     1160     1170     1180     1190     1200
      *      *      *      *      *
CTTGCATGAG GAGGAGCATG TCCTGCTCAT GGCCATCTGC ATCGTCTCCC
GAACGTACTC CTCCTCGTAC AGGACGAGTA CCGGTAGACG TAGCAGAGGG
LeuHisGlu GluGluHis ValLeuLeuMet AlaIleCys IleValSer>

     1210     1220     1230     1240     1250
      *      *      *      *      *
CAGATCGTCC TGGGGTGCAG GACGCCGCGC TGATTGAGGC CATCCAGGAC
GTCTAGCAGG ACCCCACGTC CTGCGGCGCG ACTAACTCCG GTAGGTCCTG
ProAspArgPro GlyValGln AspAlaAla LeuIleGluAla IleGlnAsp>

     1260     1270     1280     1290     1300
      *      *      *      *      *
CGCCTGTCCA ACACACTGCA GACGTACATC CGCTGCCGCC ACCCGCCCCC
GCGGACAGGT TGTGTGACGT CTGCATGTAG GCGACGGCGG TGGGCGGGGG
ArgLeuSer AsnThrLeuGln ThrTyrIle ArgCysArg HisProProPro>

```



## FIG. 5D

```
      1310      1320      1330      1340      1350
      *      *      *      *      *      *      *
GGGCAGCCAC CTGCTCTATG CCAAGATGAT CCAGAAGCTA GCCGACCTGC
CCCGTCGGTG GACGAGATAC GGTCTCTACTA GGTCTTCGAT CGGCTGGACG
GlySerHis LeuLeuTyr AlaLysMetIle GlnLysLeu AlaAspLeu>

      1360      1370      1380      1390      1400
      *      *      *      *      *      *      *
GCAGCCTCAA TGAGGAGCAC TCCAAGCAGT ACCGCTGCCT CTCCTTCCAG
CGTCGGAGTT ACTCCTCGTG AGGTTCGTCA TGGCGACGGA GAGGAAGGTC
ArgSerLeuAsn GluGluHis SerLysGln TyrArgCysLeu SerPheGln>

      1410      1420      1430      1440      1450
      *      *      *      *      *      *      *
CCTGAGTGCA GCATGAAGCT AACGCCCTT GTGCTCGAAG TGTTTGGCAA
GGACTCACGT CGTACTTCGA TTGCGGGGAA CACGAGCTTC ACAAACCGTT
ProGluCys SerMetLysLeu ThrProLeu ValLeuGlu ValPheGlyAsn>

      1460
      *      *
TGAGATCTCC TGA (SEQ ID NO:2)
ACTCTAGAGG ACT (SEQ ID NO:17)
GluIleSer ***>(SEQ ID NO:9)
```

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## FIG. 6A

### Transcript 9

(Sequence range: 1 to 1382)

```

      10      20      30      40      50
      *      *      *      *      *
GTTTCCTTCT TCTGTCGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
                                   MetGluTrpArg AsnLysLys>

      60      70      80      90     100
      *      *      *      *      *
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGGGAT
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCCCTA
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGlyMet>

     110     120     130     140     150
      *      *      *      *      *
GGAGGCAATG GCGGCCAGCA CTTCCCTGCC TGACCCTGGA GACTTTGACC
CCTCCGTTAC CGCCGGTCGT GAAGGGACGG ACTGGGACCT CTGAAACTGG
GluAlaMet AlaAlaSer ThrSerLeuPro AspProGly AspPheAsp>

     160     170     180     190     200
      *      *      *      *      *
GGAACGTGCC CCGGATCTGT GGGGTGTGTG GAGACCGAGC CACTGGCTTT
CCTTGACACGG GGCCTAGACA CCCACACAC CTCTGGCTCG GTGACCGAAA
ArgAsnValPro ArgIleCys GlyValCys GlyAspArgAla ThrGlyPhe>

     210     220     230     240     250
      *      *      *      *      *
CACTTCAATG CTATGACCTG TGAAGGCTGC AAAGGCTTCT TCAGGCGAAG
GTGAAGTTAC GATACTGGAC ACTTCCGACG TTTCCGAAGA AGTCCGCTTC
HisPheAsn AlaMetThrCys GluGlyCys LysGlyPhe PheArgArgSer>

     260     270     280     290     300
      *      *      *      *      *
CATGAAGCGG AAGGCACTAT TCACCTGCCC CTTCAACGGG GACTGCCGCA
GTACTTCGCC TTCCGTGATA AGTGGACGGG GAAGTTGCCC CTGACGGCGT
MetLysArg LysAlaLeu PheThrCysPro PheAsnGly AspCysArg>

     310     320     330     340     350
      *      *      *      *      *
TCACCAAGGA CAACCGACGC CACTGCCAGG CCTGCCGGCT CAAACGCTGT
AGTGGTTCCCT GTTGGCTGCG GTGACGGTCC GGACGGCCGA GTTTGCGACA
IleThrLysAsp AsnArgArg HisCysGln AlaCysArgLeu LysArgCys>

     360     370     380     390     400
      *      *      *      *      *
GTGGACATCG GCATGATGAA GGAGTTCATT CTGACAGATG AGGAAGTGCA
CACCTGTAGC CGTACTACTT CCTCAAGTAA GACTGTCTAC TCCTTCACGT
ValAspIle GlyMetMetLys GluPheIle LeuThrAsp GluGluValGln>

```



JUL 15 2003

## FIG. 6B

```

      410      420      430      440      450
      *      *      *      *      *
GAGGAAGCGG GAGATGATCC TGAAGCGGAA GGAGGAGGAG GCCTTGAAGG
CTCCTTCGCC CTCTACTAGG ACTTCGCCTT CCTCCTCCTC CGGAACTTCC
  ArgLysArg GluMetIle LeuLysArgLys GluGluGlu AlaLeuLys>

      460      470      480      490      500
      *      *      *      *      *
ACAGTCTGCG GCCCAAGCTG TCTGAGGAGC AGCAGCGCAT CATTGCCATA
TGTCAGACGC CGGGTTCGAC AGACTCCTCG TCGTCGCGTA GTAACGGTAT
AspSerLeuArg ProLysLeu SerGluGlu GlnGlnArgIle IleAlaIle>

      510      520      530      540      550
      *      *      *      *      *
CTGCTGGACG CCCACCATAA GACCTACGAC CCCACCTACT CCGACTTCTG
GACGACCTGC GGGTGGTATT CTGGATGCTG GGGTGGATGA GGCTGAAGAC
LeuLeuAsp AlaHisHisLys ThrTyrAsp ProThrTyr SerAspPheCys>

      560      570      580      590      600
      *      *      *      *      *
CCAGTTCCGG CCTCCAGTTC GTGTGAATGA TGGTGGAGGG AGCCATCCTT
GGTCAAGGCC GGAGGTCAAG CACACTTACT ACCACCTCCC TCGGTAGGAA
  GlnPheArg ProProVal ArgValAsnAsp GlyGlyGly SerHisPro>

      610      620      630      640      650
      *      *      *      *      *
CCAGGCCCAA CTCCAGACAC ACTCCCAGCT TCTCTGGGGA CTCCTCCTCC
GGTCCGGGTT GAGGTCTGTG TGAGGGTCGA AGAGACCCCT GAGGAGGAGG
SerArgProAsn SerArgHis ThrProSer PheSerGlyAsp SerSerSer>

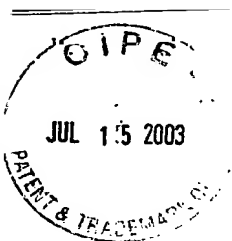
      660      670      680      690      700
      *      *      *      *      *
TCCTGCTCAG ATCACTGTAT CACCTCTTCA GACATGATGG ACTCGTCCAG
AGGACGAGTC TAGTGACATA GTGGAGAAGT CTGTACTACC TGAGCAGGTC
SerCysSer AspHisCysIle ThrSerSer AspMetMet AspSerSerSer>

      710      720      730      740      750
      *      *      *      *      *
CTTCTCCAAT CTGGATCTGA GTGAAGAAGA TTCAGATGAC CCTTCTGTGA
GAAGAGGTTA GACCTAGACT CACTTCTTCT AAGTCTACTG GGAAGACACT
  PheSerAsn LeuAspLeu SerGluGluAsp SerAspAsp ProSerVal>

      760      770      780      790      800
      *      *      *      *      *
CCCTAGAGCT GTCCCAGCTC TCCATGCTGC CCCACCTGGC TGACCTGGTC
GGGATCTCGA CAGGGTCGAG AGGTACGACG GGGTGGACCG ACTGGACCAG
ThrLeuGluLeu SerGlnLeu SerMetLeu ProHisLeuAla AspLeuVal>

      810      820      830      840      850
      *      *      *      *      *
AGTTACAGCA TCCAAAAGGT CATTGGCTTT GCTAAGATGA TACCAGGATT
TCAATGTCGT AGGTTTTCCTA GTAACCGAAA CGATTCTACT ATGGTCCTAA
SerTyrSer IleGlnLysVal IleGlyPhe AlaLysMet IleProGlyPhe>

```



## FIG. 6C

```
      860      870      880      890      900
      *      *      *      *      *      *
CAGAGACCTC ACCTCTGAGG ACCAGATCGT ACTGCTGAAG TCAAGTGCCA
GTCTCTGGAG TGGAGACTCC TGGTCTAGCA TGACGACTTC AGTTCACGGT
ArgAspLeu ThrSerGlu AspGlnIleVal LeuLeuLys SerSerAla>

      910      920      930      940      950
      *      *      *      *      *      *
TTGAGGTCAT CATGTTGCGC TCCAATGAGT CCTTCACCAT GGACGACATG
AACTCCAGTA GTACAACGCG AGGTTACTCA GGAAGTGGTA CCTGCTGTAC
IleGluValIle MetLeuArg SerAsnGlu SerPheThrMet AspAspMet>

      960      970      980      990     1000
      *      *      *      *      *      *
TCCTGGACCT GTGGCAACCA AGACTACAAG TACCGCGTCA GTGACGTGAC
AGGACCTGGA CACCGTTGGT TCTGATGTTT ATGGCGCAGT CACTGCACTG
SerTrpThr CysGlyAsnGln AspTyrLys TyrArgVal SerAspValThr>

     1010     1020     1030     1040     1050
      *      *      *      *      *      *
CAAAGCCGGA CACAGCCTGG AGCTGATTGA GCCCCTCATC AAGTTCCAGG
GTTTCGGCCT GTGTCGGACC TCGACTAACT CGGGGAGTAG TTCAAGGTCC
LysAlaGly HisSerLeu GluLeuIleGlu ProLeuIle LysPheGln>

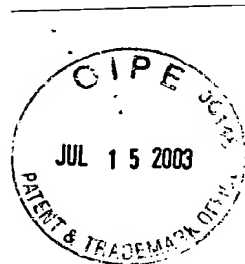
     1060     1070     1080     1090     1100
      *      *      *      *      *      *
TGGGACTGAA GAAGCTGAAC TTGCATGAGG AGGAGCATGT CCTGCTCATG
ACCCTGACTT CTTCGACTTG AACGTACTCC TCCTCGTACA GGACGAGTAC
ValGlyLeuLys LysLeuAsn LeuHisGlu GluGluHisVal LeuLeuMet>

     1110     1120     1130     1140     1150
      *      *      *      *      *      *
GCCATCTGCA TCGTCTCCCC AGATCGTCCT GGGGTGCAGG ACGCCGCGCT
CGGTAGACGT AGCAGAGGGG TCTAGCAGGA CCCCACGTCC TGCGGCGCGA
AlaIleCys IleValSerPro AspArgPro GlyValGln AspAlaAlaLeu>

     1160     1170     1180     1190     1200
      *      *      *      *      *      *
GATTGAGGCC ATCCAGGACC GCCTGTCCAA CACACTGCAG ACGTACATCC
CTAACTCCGG TAGGTCTCTG CGGACAGGTT GTGTGACGTC TGCATGTAGG
IleGluAla IleGlnAsp ArgLeuSerAsn ThrLeuGln ThrTyrIle>

     1210     1220     1230     1240     1250
      *      *      *      *      *      *
GCTGCCGCCA CCCGCCCCCG GGCAGCCACC TGCTCTATGC CAAGATGATC
CGACGGCGGT GGGCGGGGGC CCGTCGGTGG ACGAGATACG GTTCTACTAG
ArgCysArgHis ProProPro GlySerHis LeuLeuTyrAla LysMetIle>

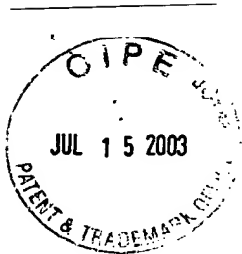
     1260     1270     1280     1290     1300
      *      *      *      *      *      *
CAGAAGCTAG CCGACCTGCG CAGCCTCAAT GAGGAGCACT CCAAGCAGTA
GTCTTCGATC GGCTGGACGC GTCGGAGTTA CTCCTCGTGA GGTTCGTCAT
GlnLysLeu AlaAspLeuArg SerLeuAsn GluGluHis SerLysGlnTyr>
```



## FIG. 6D

```
      1310      1320      1330      1340      1350
      *      *      *      *      *      *      *      *
CCGCTGCCTC TCCTTCCAGC CTGAGTGCAG CATGAAGCTA ACGCCCCTTG
GGCGACGGAG AGGAAGGTCG GACTCACGTC GTACTTCGAT TGCGGGGAAC
  ArgCysLeu SerPheGln ProGluCysSer MetLysLeu ThrProLeu>

      1360      1370      1380
      *      *      *      *      *      *
TGCTCGAAGT GTTTGGCAAT GAGATCTCCT GA (SEQ ID NO:3)
ACGAGCTTCA CAAACCGTTA CTCTAGAGGA CT (SEQ ID NO:18)
ValLeuGluVal PheGlyAsn GluIleSer ***> (SEQ ID NO:10)
```



## FIG. 7A

### Transcript 10

(Sequence Range: 1 to 1534)

10	20	30	40	50
* * * *	* * * *	* * * *	* * * *	* * * *
GTTTCCTTCT	TCTGTCCGGG	CGCCTTGGCA	TGGAGTGGAG	GAATAAGAAA
CAAAGGAAGA	AGACAGCCCC	GCGGAACCGT	ACCTCACCTC	CTTATTCTTT
MetGluTrpArg AsnLysLys>				
60	70	80	90	100
* * * *	* * * *	* * * *	* * * *	* * * *
AGGAGCGATT	GGCTGTCGAT	GGTGCTCAGA	ACTGCTGGAG	TGGAGGGGAT
TCCTCGCTAA	CCGACAGCTA	CCACGAGTCT	TGACGACCTC	ACCTCCCCTA
ArgSerAsp	TrpLeuSerMet	ValLeuArg	ThrAlaGly	ValGluGlyMet>
110	120	130	140	150
* * * *	* * * *	* * * *	* * * *	* * * *
GGAGGCAATG	GCGGCCAGCA	CTTCCCTGCC	TGACCCTGGA	GACTTTGACC
CCTCCGTTAC	CGCCGGTCGT	GAAGGGACGG	ACTGGGACCT	CTGAAACTGG
GluAlaMet	AlaAlaSer	ThrSerLeuPro	AspProGly	AspPheAsp>
160	170	180	190	200
* * * *	* * * *	* * * *	* * * *	* * * *
GGAACGTGCC	CCGGATCTGT	GGGGTGTGTG	GAGACCGAGC	CACTGGCTTT
CCTTGCACGG	GGCCTAGACA	CCCCACACAC	CTCTGGCTCG	GTGACCGAAA
ArgAsnValPro	ArgIleCys	GlyValCys	GlyAspArgAla	ThrGlyPhe>
210	220	230	240	250
* * * *	* * * *	* * * *	* * * *	* * * *
CACTTCAATG	CTATGACCTG	TGAAGGCTGC	AAAGGCTTCT	TCAGGTGAGC
GTGAAGTTAC	GATACTGGAC	ACTTCCGACG	TTTCCGAAGA	AGTCCACTCG
HisPheAsn	AlaMetThrCys	GluGlyCys	LysGlyPhe	PheArg*** (SEQ ID NO:11)
260	270	280	290	300
* * * *	* * * *	* * * *	* * * *	* * * *
CCCCCTCCCA	GGCTCTCCCC	AGTGGAAGG	GAGGGAGAAG	AAGCAAGGTG
GGGGGAGGGT	CCGAGAGGGG	TCACCTTTCC	CTCCCTCTTC	TTCGTTCCAC
310	320	330	340	350
* * * *	* * * *	* * * *	* * * *	* * * *
TTTCCATGAA	GGGAGCCCTT	GCATTTTTC	CATCTCCTTC	CTTACAATGT
AAAGGTACTT	CCCTCGGGAA	CGTAAAAAGT	GTAGAGGAAG	GAATGTTACA
360	370	380	390	400
* * * *	* * * *	* * * *	* * * *	* * * *
CCATGGAACA	TGCGGCGCTC	ACAGCCACAG	GAGCAGGAGG	GTCTTGGCGA
GGTACCTTGT	ACGCCGCGAG	TGTCGGTGT	CTCGTCCTCC	CAGAACCGCT



## FIG. 7B

410	420	430	440	450
* *	* *	* *	* *	* *
AGCATGAAGC	GGAAGGCACT	ATTCACCTGC	CCCTTCAACG	GGGACTGCCG
TCGTACTTCG	CCTTCCGTGA	TAAGTGGACG	GGGAAGTTGC	CCCTGACGGC
460	470	480	490	500
* *	* *	* *	* *	* *
CATCACCAAG	GACAACCGAC	GCCACTGCCA	GGCCTGCCGG	CTCAAACGCT
GTAGTGGTTC	CTGTTGGCTG	CGGTGACGGT	CCGGACGGCC	GAGTTTGCGA
510	520	530	540	550
* *	* *	* *	* *	* *
GTGTGGACAT	CGGCATGATG	AAGGAGTTCA	TTCTGACAGA	TGAGGAAAGTG
CACACCTGTA	GCCGTACTAC	TTCTCAAGT	AAGACTGTCT	ACTCCTTCAC
560	570	580	590	600
* *	* *	* *	* *	* *
CAGAGGAAGC	GGGAGATGAT	CCTGAAGCGG	AAGGAGGAGG	AGGCCTTGAA
GTCTCCTTCG	CCCTCTACTA	GGAATTCGCC	TTCTCCTCC	TCCGGAACCTT
610	620	630	640	650
* *	* *	* *	* *	* *
GGACAGTCTG	CGGCCCAAGC	TGTCTGAGGA	GCAGCAGCGC	ATCATTGCCA
CCTGTCAGAC	GCCGGGTTTCG	ACAGACTCCT	CGTCGTCGCG	TAGTAACGGT
660	670	680	690	700
* *	* *	* *	* *	* *
TACTGCTGGA	CGCCCACCAT	AAGACCTACG	ACCCACCTA	CTCCGACTTC
ATGACGACCT	GCGGGTGGTA	TTCTGGATGC	TGGGGTGGAT	GAGGCTGAAG
710	720	730	740	750
* *	* *	* *	* *	* *
TGCCAGTTCC	GGCCTCCAGT	TCGTGTGAAT	GATGGTGGAG	GGAGCCATCC
ACGGTCAAGG	CCGGAGGTCA	AGCACACTTA	CTACCACCTC	CCTCGGTAGG
760	770	780	790	800
* *	* *	* *	* *	* *
TTCCAGGCCC	AACTCCAGAC	ACACTCCCAG	CTTCTCTGGG	GACTCCTCCT
AAGGTCCGGG	TTGAGGTCTG	TGTGAGGGTC	GAAGAGACCC	CTGAGGAGGA
810	820	830	840	850
* *	* *	* *	* *	* *
CCTCCTGCTC	AGATCACTGT	ATCACCTCTT	CAGACATGAT	GGACTCGTCC
GGAGGACGAG	TCTAGTGACA	TAGTGGAGAA	GTCTGTACTA	CCTGAGCAGG
860	870	880	890	900
* *	* *	* *	* *	* *
AGCTTCTCCA	ATCTGGATCT	GAGTGAAGAA	GATTTCAGATG	ACCCTTCTGT
TCGAAGAGGT	TAGACCTAGA	CTCACTTCTT	CTAAGTCTAC	TGGGAAGACA
910	920	930	940	950
* *	* *	* *	* *	* *
GACCCTAGAG	CTGTCCCAGC	TCTCCATGCT	GCCCCACCTG	GCTGACCTGG
CTGGGATCTC	GACAGGGTCG	AGAGGTACGA	CGGGGTGGAC	CGACTGGACC



## FIG. 7C

960	970	980	990	1000
* *	* *	* *	* *	* *
TCAGTTACAG	CATCCAAAAG	GTCATTGGCT	TTGCTAAGAT	GATACCAGGA
AGTCAATGTC	GTAGGTTTTC	CAGTAACCGA	AACGATTCTA	CTATGGTCCT
1010	1020	1030	1040	1050
* *	* *	* *	* *	* *
TTCAGAGACC	TCACCTCTGA	GGACCAGATC	GTACTGCTGA	AGTCAAGTGC
AAGTCTCTGG	AGTGGAGACT	CCTGGTCTAG	CATGACGACT	TCAGTTCACG
1060	1070	1080	1090	1100
* *	* *	* *	* *	* *
CATTGAGGTC	ATCATGTTGC	GCTCCAATGA	GTCCTTCACC	ATGGACGACA
GTAACCTCCAG	TAGTACAACG	CGAGGTTACT	CAGGAAGTGG	TACCTGCTGT
1110	1120	1130	1140	1150
* *	* *	* *	* *	* *
TGTCCTGGAC	CTGTGGCAAC	CAAGACTACA	AGTACCGCGT	CAGTGACGTG
ACAGGACCTG	GACACCGTTG	GTTCTGATGT	TCATGGCGCA	GTCACTGCAC
1160	1170	1180	1190	1200
* *	* *	* *	* *	* *
ACCAAAGCCG	GACACAGCCT	GGAGCTGATT	GAGCCCCTCA	TCAAGTTCCA
TGGTTTCGGC	CTGTGTCGGA	CCTCGACTAA	CTCGGGGAGT	AGTTCAAGGT
1210	1220	1230	1240	1250
* *	* *	* *	* *	* *
GGTGGGACTG	AAGAAGCTGA	ACTTGCAATGA	GGAGGAGCAT	GTCCTGCTCA
CCACCCTGAC	TTCTTCGACT	TGAACGTACT	CCTCCTCGTA	CAGGACGAGT
1260	1270	1280	1290	1300
* *	* *	* *	* *	* *
TGGCCATCTG	CATCGTCTCC	CCAGATCGTC	CTGGGGTGCA	GGACGCCGCG
ACCGGTAGAC	GTAGCAGAGG	GGTCTAGCAG	GACCCACAGT	CCTGCGGCGC
1310	1320	1330	1340	1350
* *	* *	* *	* *	* *
CTGATTGAGG	CCATCCAGGA	CCGCCTGTCC	AACACACTGC	AGACGTACAT
GACTAACTCC	GGTAGGTCCT	GGCGGACAGG	TTGTGTGACG	TCTGCATGTA
1360	1370	1380	1390	1400
* *	* *	* *	* *	* *
CCGCTGCCGC	CACCCGCCCC	CGGGCAGCCA	CCTGCTCTAT	GCCAAGATGA
GGCGACGGCG	GTGGGCGGGG	GCCCGTCGGT	GGACGAGATA	CGGTCTACT
1410	1420	1430	1440	1450
* *	* *	* *	* *	* *
TCCAGAAGCT	AGCCGACCTG	CGCAGCCTCA	ATGAGGAGCA	CTCCAAGCAG
AGGTCTTCGA	TCGGCTGGAC	GCGTCGGAGT	TACTCCTCGT	GAGGTTCGTC
1460	1470	1480	1490	1500
* *	* *	* *	* *	* *
TACCGCTGCC	TCTCCTTCCA	GCCTGAGTGC	AGCATGAAGC	TAACGCCCCCT
ATGGCGACGG	AGAGGAAGGT	CGGACTCACG	TCGTACTTCG	ATTGCGGGGA



Title: Isoforms of the Human Vitamin D Receptor  
Inventor: Crofts et al.  
Application No.: 09/509,482  
Docket No.: RICE-014

## FIG. 7D

1510	1520	1530
*	*	*
TGTGCTCGAA	GTGTTTGGCA	ATGAGATCTC
CTGA (SEQ ID NO:4)		
ACACGAGCTT	CACAAACCGT	TACTCTAGAG
		GA CT (SEQ ID NO:19)



## FIG. 8A

```

      10          20          30          40          50
      *          *          *          *          *
TGCGACCTTG GCGGTGAGCC TGGGGACAGG GGTGAGGCCA GAGACGGACG
ACGCTGGAAC CGCCACTCGG ACCCCTGTCC CCACTCCGGT CTCTGCCTGC

      60          70          80          90          100
      *          *          *          *          *
GACGCAGGGG CCCGGCCCCAA GGCGAGGGAG AACAGCGGCA CTAAGGCAGA
CTGCGTCCCC GGGCCGGGTT CCGCTCCCTC TTGTCGCCGT GATTCCGTCT

      110         120         130         140         150
      *          *          *          *          *
AAGGAAGAGG GCGGTGTGTT CACCCGCAGC CCAATCCATC ACTCAGCAAC
TTCCTTCTCC CGCCACACAA GTGGGCGTCG GGTTAGGTAG TGAGTCGTTG

      160         170         180         190         200
      *          *          *          *          *
TCCTAGACGC TGGTAGAAAG TTCCTCCGAG GAGCCTGCCA TCCAGTCGTG
AGGATCTGCG ACCATCTTTC AAGGAGGCTC CTCGGACGGT AGGTCAGCAC

      210         220         230         240         250
      *          *          *          *          *
CGTGCAAGAAG CCTTTGGGTC TGAAGTGTCT GTGAGACCTC ACAGAAGAGC
GCACGTCTTC GGAAACCCAG ACTTCACAGA CACTCTGGAG TGTCTTCTCG

      260         270         280         290         300
      *          *          *          *          *
ACCCCTGGGC TCCACTTACC TGCCCCCTGC TCCTTCAGGG ATGGAGGCAA
TGGGGACCCG AGGTGAATGG ACGGGGGACG AGGAAGTCCC TACCTCCGTT
                                         MetGluAla>

      310         320         330         340         350
      *          *          *          *          *
TGGCGGCCAG CACTTCCCTG CCTGACCCTG GAGACTTTGA CCGGAACGTG
ACCGCCGGTC GTGAAGGGAC GGAAGTGGAC CTCTGAAACT GGCCTTGCAC
MetAlaAlaSer ThrSerLeu ProAspPro GlyAspPheAsp ArgAsnVal>

      360         370         380         390         400
      *          *          *          *          *
CCCCGGATCT GTGGGGTGTG TGGAGACCGA GCCACTGGCT TTCACTTCAA
GGGGCCTAGA CACCCACAC ACCTCTGGCT CGGTGACCGA AAGTGAAGTT
ProArgIle CysGlyValCys GlyAspArg AlaThrGly PheHisPheAsn>

      410         420         430         440         450
      *          *          *          *          *
TGCTATGACC TGTGAAGGCT GCAAAGGCTT CTTGAGGCGA AGCATGAAGC
ACGATACTGG ACACTTCCGA CGTTTCCGAA GAAGTCCGCT TCGTACTTCG
AlaMetThr CysGluGly CysLysGlyPhe PheArgArg SerMetLys>

      460         470         480         490         500
      *          *          *          *          *
GGAAGGCACT ATTCACCTGC CCCTTCAACG GGGACTGCCG CATCACCAAG
CCTTCCGTGA TAAGTGGACG GGAAGTTGCG CCCTGACGGC GTAGTGGTTC
ArgLysAlaLeu PheThrCys ProPheAsn GlyAspCysArg IleThrLys>

```





## FIG. 8B

```
510      520      530      540      550
*        *        *        *        *
GACAACCGAC GCCACTGCCA GGCCTGCCGG CTCAAACGCT GTGTGGACAT
CTGTTGGCTG CGGTGACGGT CCGGACGGCC GAGTTTGCGA CACACCTGTA
AspAsnArg ArgHisCysGln AlaCysArg LeuLysArg CysValAspIle>

560      570      580      590      600
*        *        *        *        *
CGGCATGATG AAGGAGTTCA TTCTGACAGA TGAGGAAGTG CAGAGGAAGC
GCCGTACTAC TTCCTCAAGT AAGACTGTCT ACTCCTTCAC GTCTCCTTCG
GlyMetMet LysGluPhe IleLeuThrAsp GluGluVal GlnArgLys>

610      620      630      640      650
*        *        *        *        *
GGGAGATGAT CCTGAAGCGG AAGGAGGAGG AGGCCTTGAA GGACAGTCTG
CCCTCTACTA GGACTTCGCC TTCCTCCTCC TCCGGAACCTT CCTGTCAGAC
ArgGluMetIle LeuLysArg LysGluGlu GluAlaLeuLys AspSerLeu>

660      670      680      690      700
*        *        *        *        *
CGGCCCCAAGC TGTCTGAGGA GCAGCAGCGC ATCATTGCCA TACTGCTGGA
GCCGGGTTCG ACAGACTCCT CGTCGTCGCG TAGTAACGGT ATGACGACCT
ArgProLys LeuSerGluGlu GlnGlnArg IleIleAla IleLeuLeuAsp>

710      720      730      740      750
*        *        *        *        *
CGCCCCACCAT AAGACCTACG ACCCCACCTA CTCCGACTTC TGCCAGTTCC
GCGGGTGGTA TTCTGGATGC TGGGGTGGAT GAGGCTGAAG ACGGTCAAGG
AlaHisHis LysThrTyr AspProThrTyr SerAspPhe CysGlnPhe>

760      770      780      790      800
*        *        *        *        *
GGCCTCCAGT TCGTGTGAAT GATGGTGGAG GGAGCCATCC TTCCAGGCCC
CCGGAGGTCA AGCACACTTA CTACCACCTC CCTCGGTAGG AAGGTCCGGG
ArgProProVal ArgValAsn AspGlyGly GlySerHisPro SerArgPro>

810      820      830      840      850
*        *        *        *        *
AACTCCAGAC AACTCCCAG CTTCTCTGGG GACTCCTCCT CCTCCTGCTC
TTGAGGTCTG TGTGAGGGTC GAAGAGACCC CTGAGGAGGA GGAGGACGAG
AsnSerArg HisThrProSer PheSerGly AspSerSer SerSerCysSer>

860      870      880      890      900
*        *        *        *        *
AGATCACTGT ATCACCTCTT CAGACATGAT GGACTCGTCC AGCTTCTCCA
TCTAGTGACA TAGTGGAGAA GTCTGTACTA CCTGAGCAGG TCGAAGAGGT
AspHisCys IleThrSer SerAspMetMet AspSerSer SerPheSer>

910      920      930      940      950
*        *        *        *        *
ATCTGGATCT GAGTGAAGAA GATTCAGATG ACCCTTCTGT GACCCTAGAG
TAGACCTAGA CTCATTCTT CTAAGTCTAC TGGGAAGACA CTGGGATCTC
AsnLeuAspLeu SerGluGlu AspSerAsp AspProSerVal ThrLeuGlu>

960      970      980      990      1000
*        *        *        *        *
CTGTCCCAGC TCTCCATGCT GCCCCACCTG GCTGACCTGG TCAGTTACAG
GACAGGGTCG AGAGGTACGA CGGGGTGGAC CGACTGGACC AGTCAATGTC
LeuSerGln LeuSerMetLeu ProHisLeu AlaAspLeu ValSerTyrSer>
```



## FIG. 8C

```
1010      1020      1030      1040      1050
      *      *      *      *      *
CATCCAAAAG GTCATTGGCT TTGCTAAGAT GATACCAGGA TTCAGAGACC
GTAGGTTTTTC CAGTAACCGA AACGATTCTA CTATGGTCCT AAGTCTCTGG
IleGlnLys ValIleGly PheAlaLysMet IleProGly PheArgAsp>

1060      1070      1080      1090      1100
      *      *      *      *      *
TCACCTCTGA GGACCAGATC GTA CTGCTGA AGTCAAGTGC CATTGAGGTC
AGTGGAGACT CCTGGTCTAG CATGACGACT TCAGTTCACG GTA ACTCCAG
LeuThrSerGlu AspGlnIle ValLeuLeu LysSerSerAla IleGluVal>

1110      1120      1130      1140      1150
      *      *      *      *      *
ATCATGTTGC GCTCCAATGA GTCCTTCACC ATGGACGACA TGTCTTGGAC
TAGTACAACG CGAGGTTACT CAGGAAGTGG TACCTGCTGT ACAGGACCTG
IleMetLeu ArgSerAsnGlu SerPheThr MetAspAsp MetSerTrpThr>

1160      1170      1180      1190      1200
      *      *      *      *      *
CTGTGGCAAC CAAGACTACA AGTACCGCGT CAGTGACGTG ACCAAAGCCG
GACACCGTTG GTTCTGATGT TCATGGCGCA GTCACTGCAC TGGTTTCGGC
CysGlyAsn GlnAspTyr LysTyrArgVal SerAspVal ThrLysAla>

1210      1220      1230      1240      1250
      *      *      *      *      *
GACACAGCCT GGAGCTGATT GAGCCCCCTCA TCAAGTTCCA GGTGGGACTG
CTGTGTCGGA CCTCGACTAA CTCGGGGAGT AGTTCAAGGT CCACCCTGAC
GlyHisSerLeu GluLeuIle GluProLeu IleLysPheGln ValGlyLeu>

1260      1270      1280      1290      1300
      *      *      *      *      *
AAGAAGCTGA ACTTGCATGA GGAGGAGCAT GTCCTGCTCA TGGCCATCTG
TTCTTCGACT TGAACGTA CTCTCTCGTA CAGGACGAGT ACCGGTAGAC
LysLysLeu AsnLeuHisGlu GluGluHis ValLeuLeu MetAlaIleCys>

1310      1320      1330      1340      1350
      *      *      *      *      *
CATCGTCTCC CCAGATCGTC CTGGGGTGCA GGACGCCGCG CTGATTGAGG
GTAGCAGAGG GGTCTAGCAG GACCCACGCT CCTGCGGCGC GACTAACTCC
IleValSer ProAspArg ProGlyValGln AspAlaAla LeuIleGlu>

1360      1370      1380      1390      1400
      *      *      *      *      *
CCATCCAGGA CCGCCTGTCC AACACACTGC AGACGTACAT CCGCTGCCGC
GGTAGGTCCT GGCGGACAGG TTGTGTGACG TCTGCATGTA GGCGACGGCG
AlaIleGlnAsp ArgLeuSer AsnThrLeu GlnThrTyrIle ArgCysArg>

1410      1420      1430      1440      1450
      *      *      *      *      *
CACCCGCCCC CGGGCAGCCA CCTGCTCTAT GCCAAGATGA TCCAGAAGCT
GTGGGCGGGG GCCCGTCGGT GGACGAGATA CGGTTCTACT AGGTCTTCGA
HisProPro ProGlySerHis LeuLeuTyr AlaLysMet IleGlnLysLeu>

1460      1470      1480      1490      1500
      *      *      *      *      *
AGCCGACCTG CGCAGCCTCA ATGAGGAGCA CTCCAAGCAG TACCGCTGCC
TCGGCTGGAC GCGTCGGAGT TACTCCTCGT GAGGTTTCGTC ATGGCGACGG
AlaAspLeu ArgSerLeu AsnGluGluHis SerLysGln TyrArgCys>
```



# FIG. 8D

1510	1520	1530	1540	1550
*	*	*	*	*
TCTCCTTCCA GCCTGAGTGC AGCATGAAGC TAACGCCCCT TGTGCTCGAA				
AGAGGAAGGT CGGACTCACG TCGTACTTCG ATTGCGGGGA ACACGAGCTT				
LeuSerPheGln ProGluCys SerMetLys LeuThrProLeu ValLeuGlu>				
1560	1570			
*	*			
GTGTTTGGCA ATGAGATCTC CTGA (SEQ ID NO:7)				
CACAAACCGT TACTCTAGAG GACT (SEQ ID NO:20)				
ValPheGly AsnGluIleSer ***> (SEQ ID NO:12)				

1510  
1520  
1530  
1540  
1550  
1560  
1570